## AGE PREDICTION OF MARINE TURTLES WITH AN EPIGENETIC CLOCK\*

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Age is a fundamental life history trait that correlates with fecundity and mortality rate. The distribution of ages in wild animal populations is therefore an important determinant of population growth rate. Unfortunately, a practical or non-lethal method to determine the age of most animals, including marine turtles, is not available yet. In this study, we present an epigenetic clock for marine turtles. This was developed using DNA extracted from skin biopsies of 63 known age (1-43 years) green sea turtles (*Chelonia mydas*) from the Cayman Islands and Réunion and further validated using wild recaptures of known time intervals. The model uses the collective DNA methylation at 18 CpG sites, also known as an epigenetic clock, and estimates age with a median absolute error of 2.1 years (2.8% of lifespan). We further used the epigenetic clock to predict the age of 250 green sea turtles across a wide range of carapace lengths (36-108cm) at Ningaloo, Western Australia. These turtles were found to be between 1-49 years of age. This enabled us to develop a population specific growth curve with predicted ages and lengths of the turtles. This study is the first to develop an epigenetic clock in a reptile and further demonstrates age can be predicted from DNA methylation across a broad variety of vertebrate species. It is also the first to use a molecular based method to characterise an age profile for a population.

NOAA Technical Memorandum NMFS-SEFSC-777 https://doi.org/10.25923/cv3r-ws82



## PROCEEDINGS OF THE FORTIETH ANNUAL SYMPOSIUM ON SEA TURTLE BIOLOGY AND CONSERVATION



40<sup>th</sup> International Sea Turtle Symposium

25 to 28 March, 2022

Perth, Australia (virtual)

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U.S. DEPARTMENT OF COMMERCE National Ocean and Atmospheric Administration National Marine Fisheries Service Southeast Fisheries Science Centre 75 Virginia Beach Drive Miami, Florida 33149

March 2024